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Corresponding author(s): Wenyi Wei

☐ Initial submission ☐ Revised version ☒ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

No statistical method was used to predetermine sample size. For cell viability assays, growth curve assays, colony formation and soft agar assays, cell migration assays and 2D/3D cell culture assays, n=3 times were included in each group to determine the statistical significance. For mouse xenograft assays, n=10 nude mice for each group were injected with indicated cell lines to ensure adequate power for statistical significance.

2. Data exclusions

Describe any data exclusions.

None of the animals was excluded from experiments.

3. Replication

Describe whether the experimental findings were reliably reproduced.

The data (except animal data) were obtained from at least three times repeated experiments. The animal data were collected and analyzed from enough mice for each group.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

For mouse xenograft assays in main Figure. 4d-f and Supplementary Figure. 8h-j, the mice were randomized and then treated with or without JQ1. (Manuscript page 21 and Supplementary Figures page 13-14).

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Investigators were not blind to group allocation during data collection and analysis because we recorded the absolute value of tumor volume and tumor weight for statistic analysis.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ A statement indicating how many times each experiment was replicated
☐	☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☒	☐ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	N/A

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	No.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	All commercial antibodies used in this study were provided in the Methods section with information regarding the dilution, vendor and catalog number (manuscript page 24).

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	The source of the cell lines were included in Methods section (manuscript page 23)
b. Describe the method of cell line authentication used.	The cell lines used in this study have not been authenticated.
c. Report whether the cell lines were tested for mycoplasma contamination.	No mycoplasma contamination was observed.
d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	No commonly misidentified cell lines were used in this study.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	Male nude mice from Taconic Biosciences were used for Xenograft assays in this study.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	Relevant information of patient samples was provided in the Methods section (manuscript page 28).